



PCT10

RAW SEQUENCE LISTING

DATE: 05/12/2003

PATENT APPLICATION: US/10/049,473A

TIME: 11:37:58

Input Set : A:\294-120PCT-US sequence listing.txt

Output Set: N:\CRF4\05122003\J049473A.raw

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3 <110> APPLICANT: de Groot, Ronald
4 Hermans, Peter Wilhelmus Maria
6 <120> TITLE OF INVENTION: Pneumococcal Vaccines
8 <130> FILE REFERENCE: Docket 294-120 PCT/US
10 <140> CURRENT APPLICATION NUMBER: US 10/049,473A
11 <141> CURRENT FILING DATE: 2002-02-12
13 <150> PRIOR APPLICATION NUMBER: PCT/NL00/00569
14 <151> PRIOR FILING DATE: 2000-08-14
16 <150> PRIOR APPLICATION NUMBER: EP 99202640.1
17 <151> PRIOR FILING DATE: 1999-08-13
19 <160> NUMBER OF SEQ ID NOS: 5
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 966
25 <212> TYPE: DNA
26 <213> ORGANISM: Streptococcus pneumoniae
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31 ctattatcag tagcaacttt agcagcttgt tcgaaagggc cagaagggtgc agacottatc 120
33 agcatgaaag gggatgtcat tacagaacat caattttatg agcaagtga aagcaaccct 180
35 tcagcccaac aagtcttgtt aaatatgacc atccaaaaag tttttgaaa acaatatggc 240
37 tcagagcttg atgataaaga ggttgatgat actattgccg aagaaaaaaa acaatatggc 300
39 gaaaactacc aacgtgtctt gtcacaagca ggtatgactc ttgaaacacg taaagctcaa 360
41 attcgtacaa gtaaattagt tgagttggca gttaagaagg tagcagaagc tgaattgaca 420
43 gatgaagcct ataagaaagc ctttgatgag tacactccag atgtaacggc tcaaatcatc 480
45 cgtcttaata atgaagataa ggccaaagaa gttctcgaaa aagccaaggc agaagggtgct 540
47 gattttgctc aattagccaa agataattca actgatgaaa aaacaaaaga aaatggtgga 600
49 gaaattacct ttgattctgc ttcaacagaa gtacctgagc aagtcaaaaa agccgctttc 660
51 gcttttagatg tggatggtgt ttctgatgtg attacagcaa ctggcacaca agcctacagt 720
53 agccaatatt acattgtaaa actcactaag aaaacagaaa aatcatctaa tattgatgac 780
55 tacaaagaaa aattaaaaac tgttatcttg actcaaaaac aaaatgattc aacatttggt 840
57 caaagcatta tcggaaaaga attgcaagca gccaatatca aggttaagga ccaagccttc 900
59 caaaatatct ttaccaata tatcgggtggt ggagattcaa gctcaagcag tagtacatca 960
61 aacgaa
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65 <211> LENGTH: 322
66 <212> TYPE: PRT
67 <213> ORGANISM: Streptococcus pneumoniae
69 <400> SEQUENCE: 2
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72 1 5 10 15
75 Gly Ala Ile Thr Leu Leu Ser Val Ala Thr Leu Ala Ala Cys Ser Lys
76 20 25 30

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79 Gly Ser Glu Gly Ala Asp Leu Ile Ser Met Lys Gly Asp Val Ile Thr
80      35      40      45
83 Glu His Gln Phe Tyr Glu Gln Val Lys Ser Asn Pro Ser Ala Gln Gln
84      50      55      60
87 Val Leu Leu Asn Met Thr Ile Gln Lys Val Phe Glu Lys Gln Tyr Gly
88 65      70      75      80
91 Ser Glu Leu Asp Asp Lys Glu Val Asp Asp Thr Ile Ala Glu Glu Lys
92      85      90      95
95 Lys Gln Tyr Gly Glu Asn Tyr Gln Arg Val Leu Ser Gln Ala Gly Met
96      100     105     110
99 Thr Leu Glu Thr Arg Lys Ala Gln Ile Arg Thr Ser Lys Leu Val Glu
100     115     120     125
103 Leu Ala Val Lys Lys Val Ala Glu Ala Glu Leu Thr Asp Glu Ala Tyr
104     130     135     140
107 Lys Lys Ala Phe Asp Glu Tyr Thr Pro Asp Val Thr Ala Gln Ile Ile
108 145     150     155     160
111 Arg Leu Asn Asn Glu Asp Lys Ala Lys Glu Val Leu Glu Lys Ala Lys
112     165     170     175
115 Ala Glu Gly Ala Asp Phe Ala Gln Leu Ala Lys Asp Asn Ser Thr Asp
116     180     185     190
119 Glu Lys Thr Lys Glu Asn Gly Gly Glu Ile Thr Phe Asp Ser Ala Ser
120     195     200     205
123 Thr Glu Val Pro Glu Gln Val Lys Lys Ala Ala Phe Ala Leu Asp Val
124     210     215     220
127 Asp Gly Val Ser Asp Val Ile Thr Ala Thr Gly Thr Gln Ala Tyr Ser
128 225     230     235     240
131 Ser Gln Tyr Tyr Ile Val Lys Leu Thr Lys Lys Thr Glu Lys Ser Ser
132     245     250     255
135 Asn Ile Asp Asp Tyr Lys Glu Lys Leu Lys Thr Val Ile Leu Thr Gln
136     260     265     270
139 Lys Gln Asn Asp Ser Thr Phe Val Gln Ser Ile Ile Gly Lys Glu Leu
140     275     280     285
143 Gln Ala Ala Asn Ile Lys Val Lys Asp Gln Ala Phe Gln Asn Ile Phe
144     290     295     300
147 Thr Gln Tyr Ile Gly Gly Asp Ser Ser Ser Ser Ser Ser Thr Ser
148 305     310     315     320
151 Asn Glu
155 <210> SEQ ID NO: 3
156 <211> LENGTH: 299
157 <212> TYPE: PRT
158 <213> ORGANISM: Lactobacillus paracasei
160 <400> SEQUENCE: 3
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166 Ala Leu Leu Leu Leu Ser Gly Cys Gln Ser Asn Gln Ala Asp Gln Lys
167     20     25     30
170 Val Ala Thr Tyr Ser Gly Gly Lys Val Thr Glu Ser Asn Phe Tyr Lys
171     35     40     45
174 Glu Leu Lys Gln Ser Pro Thr Thr Lys Thr Met Leu Ala Asn Met Leu

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175      50      55      60
178 Ile Tyr Arg Ala Leu Asn His Ala Tyr Gly Lys Ser Val Ser Thr Lys
179 65      70      75      80
182 Thr Val Asn Asp Ala Tyr Asp Ser Tyr Lys Gln Gln Tyr Gly Glu Asn
183      85      90      95
186 Phe Asp Ala Phe Leu Ser Gln Asn Gly Phe Ser Arg Ser Ser Phe Lys
187      100      105      110
190 Glu Ser Leu Arg Thr Asn Phe Leu Ser Glu Val Ala Leu Lys Lys Leu
191      115      120      125
194 Lys Lys Val Ser Glu Ser Gln Leu Lys Ala Val Trp Lys Thr Tyr Gln
195      130      135      140
198 Pro Lys Val Thr Val Gln His Ile Leu Thr Ser Asp Glu Asp Thr Ala
199 145      150      155      160
202 Lys Gln Val Ile Ser Asp Leu Ala Ala Gly Lys Asp Phe Ala Thr Leu
203      165      170      175
206 Ala Lys Thr Asp Ser Ile Asp Thr Ala Thr Lys Asp Asn Gly Gly Lys
207      180      185      190
210 Ile Ser Phe Glu Ser Asn Asn Lys Thr Leu Asp Ala Thr Phe Lys Asp
211      195      200      205
214 Ala Ala Tyr Lys Leu Lys Asn Gly Asp Tyr Thr Gln Thr Pro Val Lys
215      210      215      220
218 Val Thr Asn Gly Tyr Glu Val Ile Lys Met Ile Asn His Pro Ala Lys
219 225      230      235      240
222 Gly Thr Phe Thr Ser Ser Lys Lys Ala Leu Thr Ala Ser Val Tyr Ala
223      245      250      255
226 Lys Trp Ser Arg Asp Ser Ser Ile Met Gln Arg Val Ile Ser Gln Val
227      260      265      270
230 Leu Lys Asn Gln His Val Thr Ile Lys Asp Lys Asp Leu Ala Asp Ala
231      275      280      285
234 Leu Asp Ser Tyr Lys Lys Pro Ala Thr Thr Asn
235      290      295
238 <210> SEQ ID NO: 4
239 <211> LENGTH: 299
240 <212> TYPE: PRT
241 <213> ORGANISM: Lactococcus lactis lactis
243 <400> SEQUENCE: 4
245 Met Lys Lys Lys Met Arg Leu Lys Val Leu Leu Ala Ser Thr Ala Thr
246 1      5      10      15
249 Ala Leu Leu Leu Leu Ser Gly Cys Gln Ser Asn Gln Thr Asp Gln Thr
250      20      25      30
253 Val Ala Thr Tyr Ser Gly Gly Lys Val Thr Glu Ser Ser Phe Tyr Lys
254      35      40      45
257 Glu Leu Lys Gln Ser Pro Thr Thr Lys Thr Met Leu Ala Asn Met Leu
258      50      55      60
261 Ile Tyr Arg Ala Leu Asn His Ala Tyr Gly Lys Ser Val Ser Thr Lys
262 65      70      75      80
265 Thr Val Asn Asp Ala Tyr Asp Ser Tyr Lys Gln Gln Tyr Gly Glu Asn
266      85      90      95
269 Phe Asp Ala Phe Leu Ser Gln Asn Gly Phe Ser Arg Ser Ser Phe Lys

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270          100          105          110
273 Glu Ser Leu Arg Thr Asn Phe Leu Ser Glu Val Ala Leu Lys Lys Leu
274          115          120          125
277 Lys Lys Val Ser Glu Ser Gln Leu Lys Ala Ala Trp Lys Thr Tyr Gln
278          130          135          140
281 Pro Lys Val Thr Val Gln His Ile Leu Thr Ser Asp Glu Asp Thr Ala
282 145          150          155          160
285 Lys Gln Val Ile Ser Asp Leu Ala Ala Gly Lys Asp Phe Ala Met Leu
286          165          170          175
289 Ala Lys Thr Asp Ser Ile Asp Thr Ala Thr Lys Asp Asn Gly Gly Lys
290          180          185          190
293 Ile Ser Phe Glu Leu Asn Asn Lys Thr Leu Asp Ala Thr Phe Lys Asp
294          195          200          205
297 Ala Ala Tyr Lys Leu Lys Asn Gly Asp Tyr Thr Gln Thr Pro Val Lys
298          210          215          220
301 Val Thr Asp Gly Tyr Glu Val Ile Lys Met Ile Asn His Pro Ala Lys
302 225          230          235          240
305 Gly Thr Phe Thr Ser Lys Lys Ala Leu Thr Ala Ser Val Tyr Ala
306          245          250          255
309 Lys Trp Ser Arg Asp Ser Ser Ile Met Gln Arg Val Ile Ser Gln Val
310          260          265          270
313 Leu Lys Asn Gln His Val Thr Ile Lys Asp Lys Asp Leu Ala Asp Ala
314          275          280          285
317 Leu Asp Ser Tyr Lys Lys Leu Ala Thr Thr Asn
318          290          295
321 <210> SEQ ID NO: 5
322 <211> LENGTH: 299
323 <212> TYPE: PRT
324 <213> ORGANISM: Lactococcus lactis cremoris
326 <400> SEQUENCE: 5
328 Met Lys Lys Lys Met Arg Leu Lys Val Leu Leu Ala Ser Thr Ala Thr
329 1          5          10          15
332 Ala Leu Leu Leu Leu Ser Gly Cys Gln Ser Asn Gln Thr Asp Gln Thr
333          20          25          30
336 Val Ala Thr Tyr Ser Gly Gly Lys Val Thr Glu Ser Ser Leu Tyr Lys
337          35          40          45
340 Glu Leu Lys Gln Ser Pro Thr Thr Lys Thr Met Leu Ala Asn Met Leu
341          50          55          60
344 Ile Tyr Arg Ala Leu Asn His Ala Tyr Gly Lys Ser Val Ser Thr Lys
345 65          70          75          80
348 Thr Val Asn Asp Ala Tyr Asp Ser Tyr Lys Gln Gln Tyr Gly Glu Asn
349          85          90          95
352 Phe Asp Ala Phe Leu Ser Gln Asn Gly Phe Ser Arg Ser Ser Phe Lys
353          100          105          110
356 Glu Ser Leu Arg Thr Asn Phe Leu Ser Glu Val Ala Leu Lys Lys Leu
357          115          120          125
360 Lys Lys Val Ser Glu Ser Gln Leu Lys Ala Ala Trp Lys Thr Tyr Gln
361          130          135          140
364 Pro Lys Val Thr Val Gln His Ile Leu Thr Ser Asp Glu Asp Thr Ala

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```

365 145                      150                      155                      160
368 Lys Gln Val Ile Ser Asp Leu Ala Ala Gly Lys Asp Phe Ala Met Leu
369                      165                      170                      175
372 Ala Lys Thr Asp Ser Ile Asp Thr Ala Thr Lys Asp Asn Gly Gly Lys
373                      180                      185                      190
376 Ile Ser Phe Glu Leu Asn Asn Lys Thr Leu Asp Ala Thr Phe Lys Asp
377                      195                      200                      205
380 Ala Ala Tyr Lys Leu Lys Asn Gly Asp Tyr Thr Gln Thr Pro Val Lys
381                      210                      215                      220
384 Val Thr Asp Gly Tyr Glu Val Ile Lys Met Ile Asn His Pro Ala Lys
385 225                      230                      235                      240
388 Gly Thr Phe Thr Ser Ser Lys Lys Ala Leu Thr Ala Ser Val Tyr Ala
389                      245                      250                      255
392 Lys Trp Ser Arg Asp Ser Ser Ile Met Gln Arg Val Ile Ser Gln Val
393                      260                      265                      270
396 Leu Lys Asn Gln His Val Thr Ile Lys Asp Lys Asp Leu Ala Asp Ala
397                      275                      280                      285
400 Leu Asp Ser Tyr Lys Lys Leu Ala Thr Thr Asn
401                      290                      295

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VERIFICATION SUMMARY

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